```
                .         .         .         .         .         .
  1  ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG   60
  1  M  S  S  R  I  A  R  A  L  A  L  V  V  T  L  L  H  L  T  R     20

                .         .         .         .         .         .
 61  CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG  120
 21  L  A  L  S  T  C  P  A  A  C  H  C  P  L  E  A  P  K  C  A     40

                .         .         .         .         .         .
121  CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC  180
 41  P  G  V  G  L  V  R  D  G  C  G  C  C  K  V  C  A  K  Q  L     60

                .         .         .         .         .         .
181  AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC  240
 61  N  E  D  C  S  K  T  Q  P  C  D  H  T  K  G  L  E  C  N  F     80

                .         .         .         .         .         .
241  GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT  300
 81  G  A  S  S  T  A  L  K  G  I  C  R  A  Q  S  E  G  R  P  C    100

                .         .         .         .         .         .
301  GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG  360
101  E  Y  N  S  R  I  Y  Q  N  G  E  S  F  Q  P  N  C  K  H  Q    120

                .         .         .         .         .         .
361  TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC  420
121  C  T  C  I  D  G  A  V  G  C  I  P  L  C  P  Q  E  L  S  L    140

                .         .         .         .         .         .
421  CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG  480
141  P  N  L  G  C  P  N  P  R  L  V  K  V  T  G  Q  C  C  E  E    160

                .         .         .         .         .         .
481  TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC  540
161  W  V  C  D  E  D  S  I  K  D  P  M  E  D  Q  D  G  L  L  G    180

                .         .         .         .         .         .
541  AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA  600
181  K  E  L  G  F  D  A  S  E  V  E  L  T  R  N  N  E  L  I  A    200

                .         .         .         .         .         .
601  GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA  660
201  V  G  K  G  S  S  L  K  R  L  P  V  F  G  M  E  P  R  I  L    220
```

FIG.1A

```
                .         .         .         .         .         .
661   TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA   720
221   Y  N  P  L  Q  G  Q  K  C  I  V  Q  T  T  S  W  S  Q  C  S     240

                .         .         .         .         .         .
721   AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT   780
241   K  T  C  G  T  G  I  S  T  R  V  T  N  D  N  P  E  C  R  L     260

                .         .         .         .         .         .
781   GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG   840
261   V  K  E  T  R  I  C  E  V  R  P  C  G  Q  P  V  Y  S  S  L     280

                .         .         .         .         .         .
841   AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC   900
281   K  K  G  K  K  C  S  K  T  K  K  S  P  E  P  V  R  F  T  Y     300

                .         .         .         .         .         .
901   GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC   960
301   A  G  C  L  S  V  K  K  Y  R  P  K  Y  C  G  S  C  V  D  G     320

                .         .         .         .         .         .
961   CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG   1020
321   R  C  C  T  P  Q  L  T  R  T  V  K  M  R  F  R  C  E  D  G     340

                .         .         .         .         .         .
1021  GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG   1080
341   E  T  F  S  K  N  V  M  M  I  Q  S  C  K  C  N  Y  N  C  P     360

                .         .         .         .         .         .
1081  CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG   1140
361   H  A  N  E  A  A  F  P  F  Y  R  L  F  N  D  I  H  K  F  R     380
1141  GACTAA  1146
381   D  *    382
```

FIG. 1B

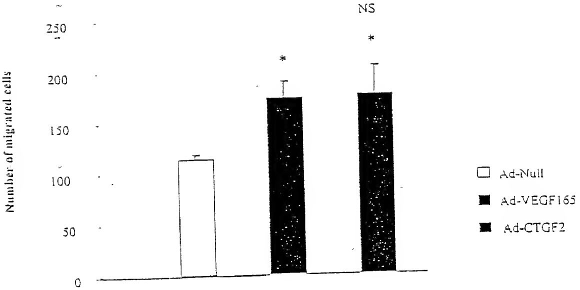
Number of migrated cells
250
200
150
100
50
0
NS
*
*
☐ Ad-Null
■ Ad-VEGF165
■ Ad-CTGF2

FIG. 2

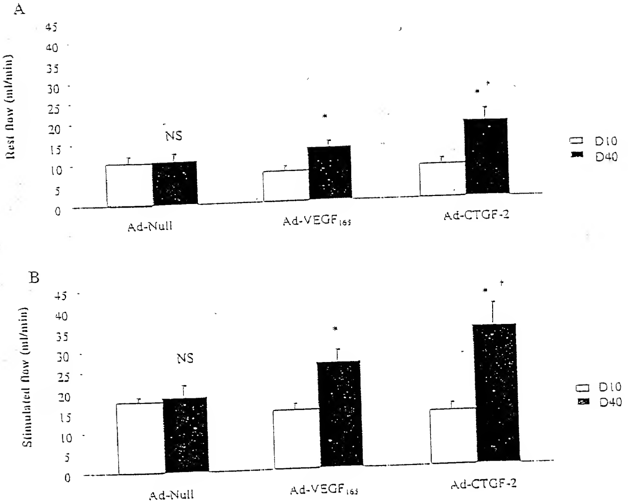
A
Rest flow (ml/min)
0
5
10
15
20
25
30
35
40
45
NS
*
* †
Ad-Null
Ad-VEGF165
Ad-CTGF-2
☐ D10
■ D40
B
Stimulated flow (ml/min)
0
5
10
15
20
25
30
35
40
45
NS
*
* †
Ad-Null
Ad-VEGF165
Ad-CTGF-2
☐ D10
■ D40

FIG. 3

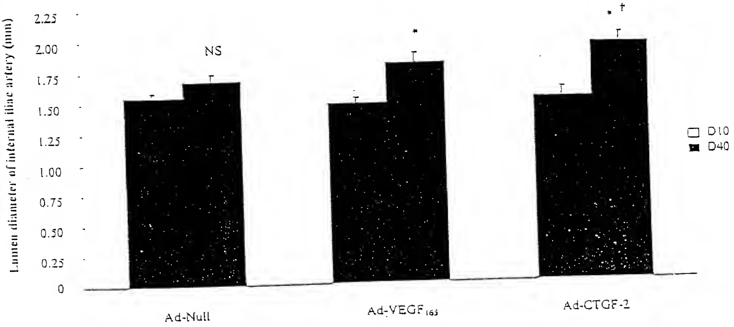
Lumen diameter of internal iliac artery (mm)
2.25
2.00
1.75
1.50
1.25
1.00
0.75
0.50
0.25
0
NS
*
* †
☐ D10
■ D40
Ad-Null
Ad-VEGF$_{165}$
Ad-CTGF-2

FIG. 4

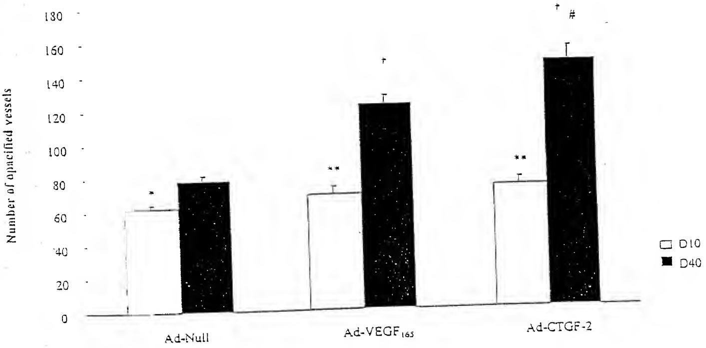
Number of opacified vessels
180
160
140
120
100
80
60
40
20
0
*
**
**
†
† #
Ad-Null
Ad-VEGF165
Ad-CTGF-2
☐ D10
■ D40

FIG. 5

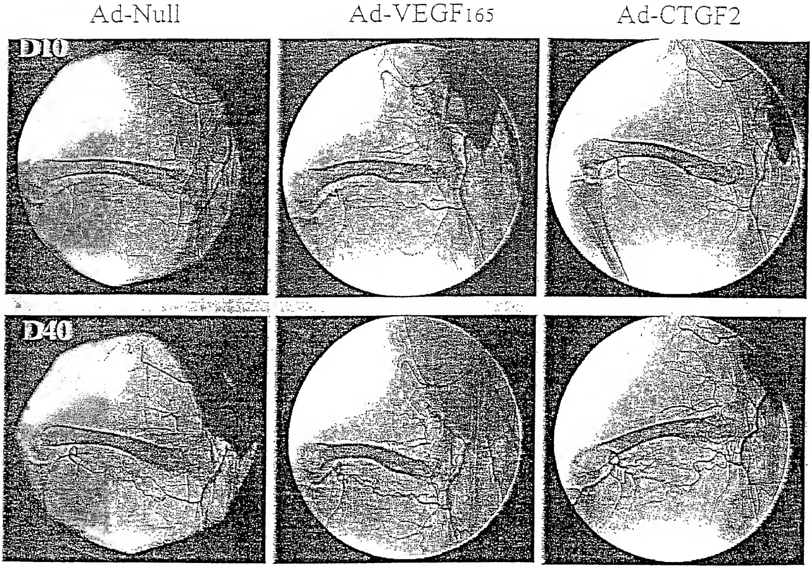

FIG. 6

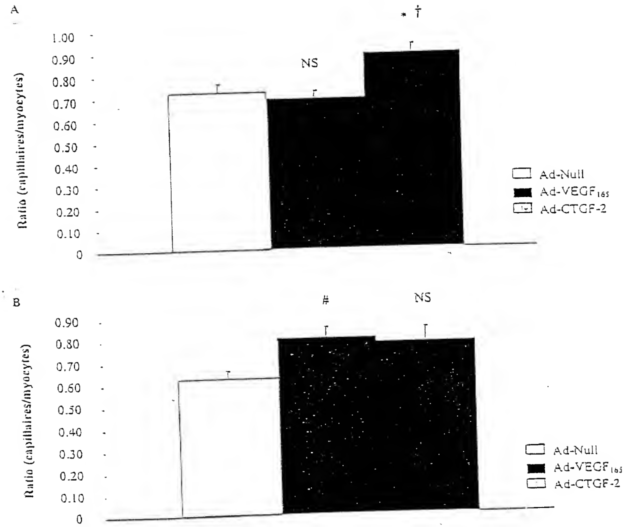
A
Ratio (capillaires/myocytes)
1.00
0.90
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0
NS
* †
□ Ad-Null
■ Ad-VEGF165
□ Ad-CTGF-2
B
Ratio (capillaires/myocytes)
0.90
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0
#
NS
□ Ad-Null
■ Ad-VEGF165
□ Ad-CTGF-2

FIG. 7

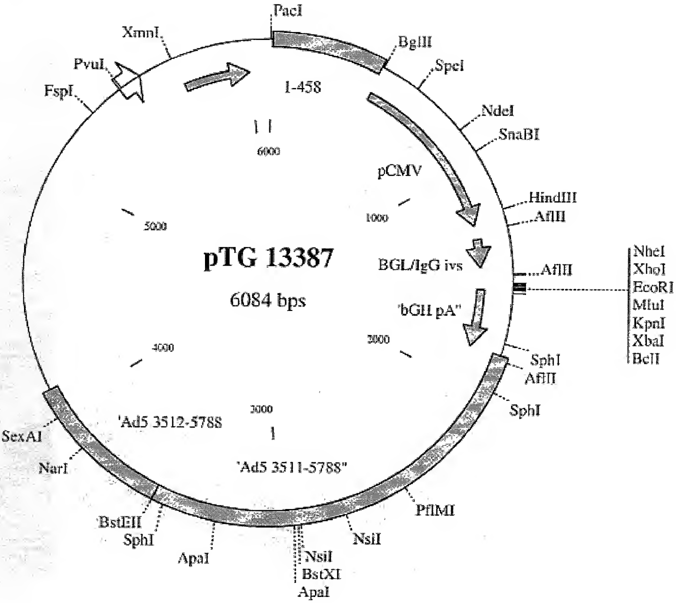
PacI
BglII
SpeI
NdeI
SnaBI
HindIII
AflII
AflII
NheI
XhoI
EcoRI
MluI
KpnI
XbaI
BclI
SphI
AflII
SphI
PflMI
NsiI
NsiI
BstXI
ApaI
ApaI
SphI
BstEII
NarI
SexAI
FspI
PvuI
XmnI
1-458
6000
pCMV
1000
5000
pTG 13387
6084 bps
BGL/IgG ivs
'bGH pA"
2000
4000
3000
'Ad5 3512-5788
'Ad5 3511-5788"

FIG. 8

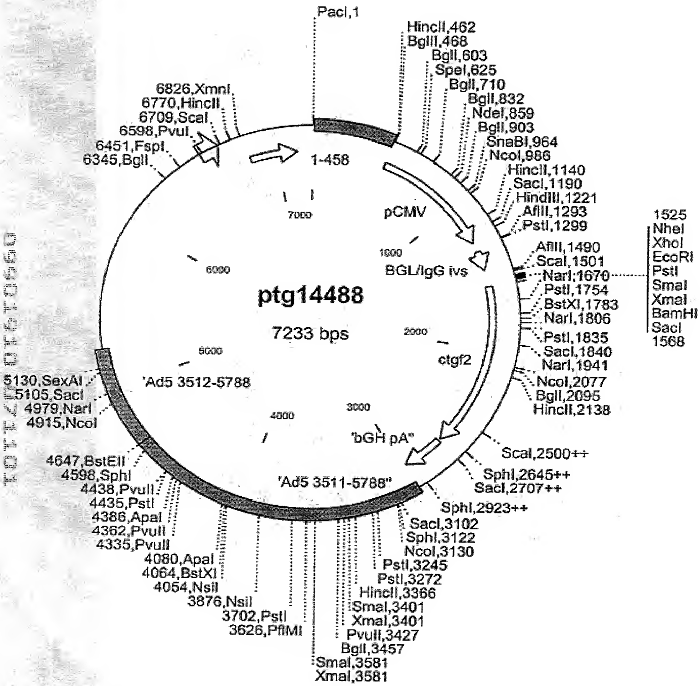
PacI,1
HincII,462
BglII,468
BglI,603
SpeI,625
BglI,710
BglI,832
NdeI,859
BglI,903
SnaBI,964
NcoI,986
HincII,1140
SacI,1190
HindIII,1221
AflII,1293
PstI,1299
AflII,1490
ScaI,1501
NarI,1670
PstI,1754
BstXI,1783
NarI,1806
PstI,1835
SacI,1840
NarI,1941
NcoI,2077
BglI,2095
HincII,2138
1525
NheI
XhoI
EcoRI
PstI
SmaI
XmaI
BamHI
SacI
1568
ScaI,2500++
SphI,2645++
SacI,2707++
SphI,2923++
SacI,3102
SphI,3122
NcoI,3130
PstI,3245
PstI,3272
HincII,3366
SmaI,3401
XmaI,3401
PvuII,3427
BglI,3457
SmaI,3581
XmaI,3581
3626,PflMI
3702,PstI
3876,NsiI
4054,NsiI
4064,BstXI
4080,ApaI
4335,PvuII
4362,PvuII
4386,ApaI
4435,PstI
4438,PvuII
4598,SphI
4647,BstEII
4915,NcoI
4979,NarI
5105,SacI
5130,SexAI
6345,BglI
6451,FspI
6598,PvuI
6709,ScaI
6770,HincII
6826,XmnI
1-458
pCMV
BGL/IgG ivs
ctgf2
'bGH pA"
'Ad5 3511-5788"
'Ad5 3512-5788
ptg14488
7233 bps
7000
1000
2000
3000
4000
5000
6000

FIG. 9

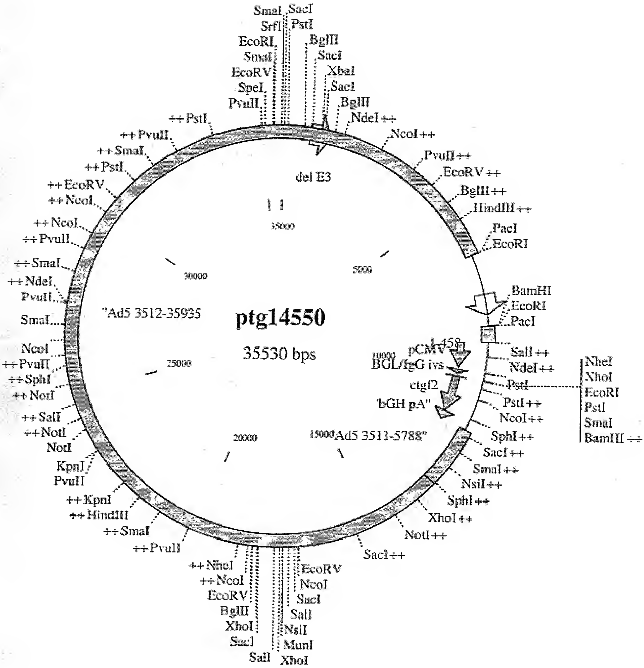
ptg14550
35530 bps
del E3
"Ad5 3512-35935
pCMV
1-458
BGL/IgG ivs
ctgf2
'bGH pA"
Ad5 3511-5788"
35000
5000
10000
15000
20000
25000
30000
SmaI
SacI
SrfI
PstI
EcoRI
BglII
SmaI
SacI
EcoRV
XbaI
SpeI
SacI
PvuII
BglII
NdeI ++
NcoI ++
PvuII ++
EcoRV ++
BglII ++
HindIII ++
PacI
EcoRI
BamHI
EcoRI
PacI
SalI ++
NdeI ++
PstI
PstI ++
NcoI ++
SphI ++
SacI ++
SmaI ++
NsiI ++
SphI ++
XhoI ++
NotI ++
SacI ++
NheI
XhoI
EcoRI
PstI
SmaI
BamHI ++
EcoRV
NcoI
SacI
SalI
NsiI
MunI
XhoI
++ NheI
++ NcoI
EcoRV
BglII
XhoI
SacI
SalI
++ PvuII
++ SmaI
++ HindIII
++ KpnI
PvuII
KpnI
NotI
++ NotI
++ SalI
++ NotI
++ SphI
++ PvuII
NcoI
SmaI
PvuII
++ NdeI
++ SmaI
++ PvuII
++ NcoI
++ NcoI
++ EcoRV
++ PstI
++ SmaI
++ PvuII
++ PstI

FIG. 10

FIG. 11A

```
ATGAGCTCCCGAATCGTCAGGGAGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG
M  S  S  R  I  V  R  E  L  A  L  V  V  T  L  L  H  L  T  R

GTGGGGCTCTCCACCTGCCCCGCTGACTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG
V  G  L  S  T  C  P  A  D  C  H  C  P  L  E  A  P  K  C  A

CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGTTGTAAGGTCTGCGCCAAGCAGCTC
P  G  V  G  L  V  R  D  G  C  G  C  C  K  V  C  A  K  Q  L

AACGAGGACTGCAGAAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC
N  E  D  C  R  K  T  Q  P  C  D  H  T  K  G  L  E  C  N  F

GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT
G  A  S  S  T  A  L  K  G  I  C  R  A  Q  S  E  G  R  P  C

GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG
E  Y  N  S  R  I  Y  Q  N  G  E  S  F  Q  P  N  C  K  H  Q

TGCACATGTATTGGATGGCGCCGGGGGGCTTGCATTCCTCTGTGTCCCCAAGAACTATCT
C  T  C  I  G  W  R  R  G  A  C  I  P  L  C  P  Q  E  L  S

CTCCCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAG
L  P  N  L  G  C  P  N  P  R  L  V  K  V  T  G  Q  C  C  E
```

MATCH WITH FIG. 11B

FIG. 11B

MATCH WITH FIG. 11A

```
GAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTT
E  W  V  C  D  E  D  S  I  K  D  P  M  E  D  Q  D  G  L  L

GGCAAGGGGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATT
G  K  G  L  G  F  D  A  S  E  V  E  L  T  R  N  N  E  L  I

GCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATC
A  V  G  K  G  S  S  L  K  R  L  P  V  F  G  M  E  P  R  I

CTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGC
L  Y  N  P  L  Q  G  Q  K  C  I  V  Q  T  T  S  W  S  Q  C

TCAAAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGC
S  K  T  C  G  T  G  I  S  T  R  V  T  N  D  N  P  E  C  R

CTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGC
L  V  K  E  T  R  I  C  E  V  R  P  C  G  Q  P  V  Y  S  S

CTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACT
L  K  K  G  K  K  C  S  K  T  K  K  S  P  E  P  V  R  F  T
```

MATCH WITH FIG. 11C

MATCH WITH FIG. 11B

FIG. 11C

```
TACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGAC
 Y  A  G  C  L  S  V  K  K  Y  R  P  K  Y  C  G  S  C  V  D

GGCCGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCCCTGCGAAGAT
 G  R  C  C  T  P  Q  L  T  R  T  V  K  M  R  F  P  C  E  D

GGGGAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTCCAAATGCAACTACAACTGC
 G  E  T  F  S  K  N  V  M  M  I  Q  S  S  K  C  N  Y  N  C

CCGCATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCCAATGA
 P  H  A  N  E  A  A  F  P  F  Y  R  L  F  Q  *
```